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OM nucleic - nucleic search, using sw model

Run on: December 13, 2002, 02:55:20 ; Search time 3610 Seconds

(without alignments)
16179.870 Million cell updates/sec

Title: US-09-716-536-7

Perfect score: 2007

Sequence: 1 gtgcgltgagcgaattg.....aaaaaaaaaaaaaaaaa 2007

Scoring table: IDENTITY NUC

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenBank: 1: gb_ba: 2: gb_bt: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_sts: 12: gb_sy: 13: gb_un: 14: gb_vl: 15: em_ba: 16: em_fun: 17: em_hum: 18: em_in: 19: em_mu: 20: em_om: 21: em_or: 22: em_ov: 23: em_pat: 24: em_ph: 25: em_pl: 26: em_ro: 27: em_sts: 28: em_un: 29: em_vl: 30: em_htg_hum: 31: em_htg_inv: 32: em_htg_other: 33: em_htg_mus: 34: em_htg_pin: 35: em_htg_rod: 36: em_htg_mam: 37: em_htg_vrl: 38: em_sy: 39: em_htgo_hum: 40: em_htgo_mus: 41: em_htgo_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2007	100.0	2007	6	AR193167	AR193167 Sequence
2	2007	100.0	2007	6	HSU77845	U77845 Human hTRIP
3	1891.2	94.2	2002	9	BC019283	BC019283 Human hTRIP
4	1891.2	94.2	2010	9	BC000310	BC000310 Homo sapi
5	1890.8	94.2	2005	6	AR072729	AR072729 Sequence
6	1890.8	94.2	2005	6	BD006990	BD006990 Modulator
7	1087	54.2	2024	10	BC017374	BC017374 Mus muscu
8	1081	53.9	1981	10	MMU77844	U77844 Mus musculu
9	1062.8	53.0	1975	6	AR193168	AR193168 Sequence
10	892.8	44.5	1781	6	AX364873	AX364873 Sequence
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21	74	3.7	39410	5	FR165K09	AJ010317 Fugu rubr
22	68.2	3.4	82400	10	AC090495	AC090495 Genomic s
23	67	3.3	195690	10	AC098726	AC098726 Mus muscu
24	65.8	3.3	7218	6	I66494	I66494 Sequence 14
25	65.4	3.3	198228	2	AC102097	AC102097 Mus muscu
26	64.6	3.2	200947	2	AC016961	AC016961 Homo sapi
27	61.8	3.1	24899	2	AC128059	AC128059 Rattus no
28	60.6	3.0	203982	9	AC067854	AC067854 Homo sapi
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32	59.6	3.0	318930	2	AC073495	AC073495 Mus muscu
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ALIGNMENTS

RESULT 1
LOCUS AR193167 2007 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7 from patent US 6346605.
ACCESSION AR193167
VERSION AR193167.1 GI:20239132
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2007)
AUTHORS Lee,S.Young, and Choi,Y.
TITLE Signal Transducer for the TNF receptor super family, and uses thereof
JOURNAL Patent: US 6346605-A 7 12-FEB-2002;

FEATURES Location/Qualifiers
source 1..2007
BASE COUNT 517 a 518 c 558 g 414 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2007; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
LOCUS HSU77845
DEFINITION Human hTRIP (hTRIP) mRNA, complete cds.
ACCESSION U77845
VERSION U77845.1
KEYWORDS GI:2039303
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS TRAF-Interacting protein (TRIP): a novel component of the tumor
necrosis factor receptor (TNFR) - and CD30-TRAF signaling complexes
TITLE that inhibits TRAF2-mediated NF-kappaB activation
JOURNAL J. Exp. Med. 185 (7), 1275-1285 (1997)
MEDLINE 97258620
PUBMED 9104814
REFERENCE 2 (bases 1 to 2007)
AUTHORS Lee, S. Y., Lee, S. Y. and Choi, Y.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-1996) Immunology, The Rockefeller University,
1230 York Avenue Box 295, New York, NY 10021, USA
FEATURES
source Location/Qualifiers
1..2007
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BASE COUNT 517 a 518 c 558 g 414 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2007; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 2010)
 Strausberg, R.
 Direct Submission
 Submitted (15-Nov-2000) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.ncl.nih.gov
 Contact: MGC help desk
 Email: c9apbs-rt@mail.nih.gov
 Tissue Procurement: DCTD/DPD
 cDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNU)
 Sequencing Center (MGC), National Institutes of Health Intramural
 Gaithersburg, Maryland;
 Web site: http://www.nisic.nih.gov/
 Contact: nisc_mgc@nih.gov
 Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
 Lim, M., Maduro, O.L., Masfello, C., Mestrian, S.D., McIlloskey, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stantirpop, S., Thomas, P.J.,
 Tjongson, E.E., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-H. and Green, E.D.

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Dh 1875 CCAACTTCTACTGCTCTTGTACTGCTCTTCTAGGATAGCTTGGGCAAGCAGGCTGGG 1934
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LOCUS AR072729 2065 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 1 from patent US 5948643.
ACCESSION AR072729
VERSION AR072729.1 GI:999493
KEYWORDS

SOURCE

Unknown.
Organism: Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 2065)

AUTHORS Rubinfield,B., Polakis,P.G., Lingenfelter,C. and Vuong,T.T.
TITLE Modulators of BRCA1 activity
JOURNAL Patent: US 5948643-A 1 07-SEP-1999;

FEATURES
Location/Qualifiers

source 1..2065

BASE COUNT 561 a 526 c 561 g 417 t

ORIGIN

Query Match 94.2%; Score 1890.8; DB 6; Length 2065;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1946; Conservative 0; Mismatches 17; Indels 5; Gaps 4;

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LOCUS	BDD06990				
DEFINITION	Modulators of BRCA1 activity.				
ACCESSION	BDD06990				
VERSION	BDD06990.1 GI:18635361				
KEYWORDS	JP 2001502893-A/L.				
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 2065)				
AUTHORS	Ludinfeld,B., Porakitsu,P., Rigenferuta,C. and Buon,T.T.				
TITLE	Modulators of BRCA1 activity				
JOURNAL	Patent: JP 2001502893-A I 06-MAR-2001;				
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COMMENT	ONIX PHARMACEUTICALS INC				
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OS	Unidentified				
PN	JP 2001502893-A/1				
PD	06-MAR-2001				
Pf	06-AUG-1997 JP 1998512659				
PR	04-SEP-1996 US 60/025601				
PI	BONY LUDINFELD, PAUL PORAKITSU, CAROL RIENFERUTA, TERLIRIN T BUON				
PC	C12N15/09,A61K38/00,A61P43/00,C07K14/435,C07K16/18,C12M1/15,				
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Best Local Similarity	98.9%;	Pred. No. 0;		
Matches 1946;	Conservative	0;	Mismatches	17; Indels 5; Gaps
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RESULT 7
BC017374 2024 bp mRNA linear ROD 07-AUG-2002
LOCUS BC017374
DEFINITION Mus musculus, TRAF-Interacting protein, clone MGC:13919
IMAGE:3990371, mRNA, complete cds.
ACCESSION BC017374
VERSION BC017374.1 GI:16924208
KEYWORDS MGC.

SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadansystemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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OY	506	TGAAAAAGCAGATGAATAGTACTTAGAGCAGCAGAGATGAGACCAACAACGACAAAGAG	565
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OY	746	GGAAGCCTCAGGGGAGGTGGCTGTACAAAGCTGAGAGGATTTGTTTTCTCTCAGAGAACA	805
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OY	806	AGTTGCACAGAGCTACTCTCTGGAATTTGGATTCAGGCCAAAGTTAAGACTGAGTCAAGCCAGA	865
Db	805	AGTTGAGAGACTCTCAACACTGAGCTGATTCAGGCCAAAGTTAAGACTGAGTCAAGCCAGA	864
OY	866	AGGACTTACAGAGTGTGTACAAAGGAATCATGTAGCCCTGAAAAAAGAGCTAAGAGATGTGC	925
Db	865	AGGACTTACAAAGTGTGTAGCCAGGAGATCATGTAGCCCTAAGAAAGAGCTGATGATCTCC	924
OY	926	AGGAAACCTTGAACCTTCCACACAGTGGCCAGTGAAGTGTTCGACCGCTGTGTTTATGAGA	985
Db	925	AGGAAACCTTGAAGCTCTCTCCGCGCACCAATGAGAGGCTCAAGCCCTGTGTTTATGAGA	984
OY	986	GCCAGAGCCCTGTGGAGGTG---AATGTGAAGTCTCGCGCGGCAATCCCTGCTGATGATA	1042
Db	985	GCCAGAGCCCTGTGGATATGATGATCAACCCAGAGCTTATACCAAGCACCTTCGGTGTATGAGA	1044
OY	1043	TTGATTCATATGCTACCTTTGATGTGATATCTCCCCAGACCCGGGCCCTTCAACTCCAGC	1102
Db	1042	TTGATTCATATGCTACCTTTGATGTGATATCTCCCCAGACCCCTTCAACTCCAGTGTCTCA	1101
OY	1103	ATGATTTACTAGAAAACCTTGGCTGTAGAGAAATGACACATCCCAATTCAGATATGTCGCCA	1162
Db	1102	ATGATTTACTCCCAAGAAACCTGTGCTGGAGAGGCGACGCTCTCCATGCAAGAAATGTCCTCA	1161
OY	1163	AGAAGATATGCAAAAGGCCCCAGAGAGAGATGCCAGCTCTACATGGGTGGACAGACTGTG	1222
Db	1162	AGAAGTGTCAACAAAGGTGTCCAAAGCCGAGATGCCAGCTCTACATGGGTGGCAGGATGTG	1221
OY	1223	CAGAGAGCCAGATGAGAGAACTGGTGTGTGCTTCCCTATTTTGTGTGCGGAATGCCATCC	1282
Db	1222		1281
OY	1225	TAGAGAGCTAGATGAGAGAACTGGCTGTGTGCTTCCCTCTCTTCAATCCGGAATGCTGTCC	1284

LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE
LOCUS 8	MMU077844	1981 bp	mRNA	linear	ROD 25-APR-1997	
DEFINITION	Mus musculus mTRIP (mTRIP) mRNA, complete cds.					
VERSION	U77844.1	GI:2039305				
KEYWORDS						
SOURCE	Mus musculus.					
ORGANISM	Mus musculus.					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
AUTHORS	Lee,S.Y., Lee,S.Y., and Choh,Y.					
TITLE	TRAF-interacting protein (TRIP): a novel component of the tumor necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes that inhibits TRAF2-mediated NF-kappaB activation					
JOURNAL	J. Exp. Med.	185 (7),	1275-1285	(1997)		
MEDLINE	97258620					
PUBMED	9104814					
REFERENCE	2 (bases 1 to 1981)					

AUTHORS Lee,S.Y., Lee,S.Y. and Choi,Y.

TITLE Direct Submission

JOURNAL Submitted (10-NOV-1996) Immunology, The Rockefeller University,

1230 York Avenue Box 295, New York, NY 10021, USA

FEATURES Location/Qualifiers

source

1..1981

/organism="Mus musculus"

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118..1530

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/translation="PIISLCTICDFPDHSDVAIHCGHTFHILQILOMETAPSR

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CKMTMEQIELLIQSRESEVEIMIDMGVGSAROLAVCYSLKEKYEAKRAT

GELADRLKDLVSSRSKLTLELDOAKLELRSAOKDLSODEITSLRKLMTILOG

TSLDPRNTNVSRLVESPAPVEMNPRLHPRPDELDLTDDVTDPVPTSGSO

HCLPKKLCLEARSBMQVNLKVKHVSPESSOLSGGRCVELDEIAGAPLFTRN

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BASE COUNT 532 a 489 c 534 g 426 t

ORIGIN

Query Match 53.9%; Score 1081; DB 10; Length 1981;

Best Local Similarity 74.6%; Pred. No. 4.7e-294;

Matches 1504; Conservative 0; Mismatches 450; Indels 63; Gaps 9;

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DB 15 GTGGCGTGGAGAAATTGAGAGAACCGAGGCGGTTCACCAAACTGTCT 74
QY 59 GTAGCAATTTCTTGGCTCCTGGGCCCTTGAGTCAGCCATCATCCTATCCGTCTC 118
DB 75 GTCTCTG-CCAGCTGTGTCCTGGGCTGCTTGAGTCAGACCATCATCCTATCCTCTC 133
QY 119 TGTGCACTATCTGCTCCGACTTCTTGATCACTCCCGCAGCGTGGCCGCTCACTGCG 178
DB 134 TGTGCACTATCTGCTCCGACTTCTTGATCACTCCCGCAGCGTGGCTGACCTGCTG 193
QY 179 GCCACACTTCCACTGCTAGTCAGTCAATTCAGTCTTGAGACAGCAGCAAGCGGACCT 238
DB 194 GCCACACTTTCATCTGCAATGCTCAATCAGTGGTTTGAGACAGCAGCAAGCGGACCT 253
QY 239 GCCACAGTGCAGAAATCCAGGTTGGCAAAAGACCATTAATCAATAAGCTCTTCTTGATC 298
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DB 614 TGGAGCAAAATTGAGCTCTCACTCAGACGACGCTCTGAGGGTGGAGGATGATTCGAG 673
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QY 959 AGACTGCAAGCCCTGTTTGTAGAGAGCCAGCCCTGTGGA--GTTGAATCTGAAGC 1015
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DB 1334 AATCCGGAAGACAGCAGATGTGTAAGATAGGCTTTGATGAGGCTTGGAGAGCAAA 1393
QY 1376 AATTCATCCAGCTACTGACACAGTATGATCCGCCATTTGCTGTTAAAGCCAGACCA 1435
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DB 1514 CTTCTCTGCTGCTGAGAAACAGTGAATGACCAATGAGTGTGCAATTA 1558
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Db	1647	CTGTGTTTACTGGCCCTGTGCACAC--ACTGGGAAGCCATATGACCAGTTTACTGTTCGG	1704
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Oy	1793	GACCTTTTCGGGCTGGAGACACAGCTACCTGTTGATCTGTCTGTGGACCA-----	18478
Db	1765	GACTCCCTTTTGTTTTATATAGAACAGGGTGCACATATGACTCTTAAGTGGATGGAGTCTCGA	18248
Oy	1848	AGTCTTGGAGCATCTCAGGCAAGCTTCAGCCCAAGCTTCTACCTGCCTTTCAGTCTGCTTC	19077
Db	1825	GGATCTCATCTCAGGCTGGAGACCTCTGCGCTTGAATCTCTGCTCTCCCTCACACTTATTCG	18844
Oy	1808	TAGCATTCAGCTGGGCCAAGCAGGCTGGGGAATGAGCATGAGCATGGGATATATGATAG	19677
Db	1885	TGTGAATATTATGGGGTGAAGTGTGTGATATGGGAAGGTGTGGGGAAGTTTCTGTGTAAATA	19447
Oy	1368	GATCGAAGATTTTCCGAAAAAAAAAAAAAAAAAAAAA 2004	
Db	1945	AAAAAGGATCTTTCTTCAAAAAAAAAAAAAAAAAAAAAA 1981	

RESULT	9				
LOCUS	AR193168				
DEFINITION	AR193168	1975 bp	DNA	linear	PAT 20-APR-2002
ACCESSION	Sequence	8 from patent US 6346605.			
VERSION	AR193168				
KEYWORDS	AR193168.1	GI:20239133			
SOURCE	.				
ORGANISM	Unknown.				
	Unknown.				

TITLE	Signal transducer for the TNF receptor super family, and uses thereof			
JOURNAL FEATURES	Patent: US 6346605-A 8 12-FEB-2002;			
source	Location/Qualifiers 1. 1975			
BASE COUNT	530 a	488 c	533 g	424 t
ORIGIN	/organism="unknown"			

Query Match	Similarity	Score	ID	Length
Best Local Similarity	74.6%	Pred. No. 6.6e-289;		
Matches 1506;	Conservative	0;	Mismatches 447;	Indels 65; Gaps 11.
QY	1	GTGCGGTGAGAGGAATTTGAAAGCAAGCGGAGCGCGGC - -GCTCTACCAAGCCGGACT	58	
Db	9	GTGCGGTGAGAGGAATTTGAAAGCAAGCGGAGCGCGGTTCCACCAACTGTGCT	68	
QY	59	GTACGATTTCTTTTGCGCTGCGCCCTTGATGTCACGCATCATGCTATCCGTGCTC	118	
Db	69	GTCTCTG - GCAGCTGTGTTCCCTCGGCGCTGTTAGTCGACCCATCATGCTATCCCTCTCTC	127	
QY	119	TGTGCATATGTCGTCGCACTCTTCGATCACTCCCGCAGCATGGCGCGGCAATCCACTGGG	178	
Db	128	TGTGCATATGTCGTCGCACTCTTCGATCACTCCCGGACGTGGCTGCATTCACACTGTG	187	
QY	179	GCCACACCTTCACATTGACAGTCGCTAATTCAGTCCCTTGAGACAGCACCAAGTCGGACCT	238	
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QY	299	TTGCGCAGAGAGAGAGATGCTTGGAATCGAGATTTCTTAAGATGAAGCTGGACAATG	358	
Db	308	TCGCCACAGAGAGAGAGATGCTTTGGATGCGAATTTCTTAAGATGAAGCTGGACAAGCG	367	
QY	359	TCAGAGCCAGCTTTCCAGAAAAGACAAGAGAGAAAGACAGACGCGCATCATCTGACA	418	

[illegible]

Dh 1447 AAGAGTAAACAGAAAGTGAATAAGACTGTGAGTTCGCTCCCAAGCAAGCTGAT 1506
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Qy 1613 CCTGAGGTGTAAAGGACAGCAACAGGTGAGGTGAGTGTGACACCCAGAGACTGCTTT 1672
Dh 1609 -----AGTCCAAAGAGATGCCCAAGAAAACACACTT 1639
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Dh 1640 CCTGTGTTTACATGCGCCCTCGCACAC--ACTGGAAAGCCACATGACCACTTACTGTGTTAC 1697
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Qy 1848 -AGTCTTGAAGCATCTGACGACGCTGACCCAGCTCTACCTGACCTTTGACTTGCTT 1906
Dh 1818 AGGATCTTATGACAGCTGAGAGACCTGCGCTTGAACTCTGCTGCTGACAGCTTATG 1877
Qy 1907 CTAGCATAGCTTGGGCCAAGCAGAGGTGGGGAATGAGATGACATGGAGTATGAGAGA 1966
Dh 1878 CTGAATATATGAGGTGAGAGTGTGTATAGGAAGTTGGGAAGTTTCTGTGTAAT 1937
Qy 1967 GGATGGAAGATTTTCCCGAAGAAAAAAGAAAAA 2004
Dh 1938 AAAAAAGGATCTTTCTTCAAAAAAAGAAAAA 1975

RESULT 10
AX364873
LOCUS AX364873 1781 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 24 from Patent WO206315.
ACCESSION AX364873
VERSION AX364873.1 GI:18696762
KEYWORDS

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1
Mintz, L., Freilich, S. and Bernstein, J.
Novel nucleic acid and amino acid sequences
Patent: WO 0206315-A 24 24-JAN-2002;

JOURNAL

CompuGen Ltd. (IL)

FEATURES

Location/Qualifiers

source

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BASE COUNT 402 a 498 c 467 g 405 t 9 others

ORIGIN

Query Match 44.5% Score 892.8; DB 6; Length 1781;
Best Local Similarity 80.9%; Pred. No. 7.7e-241;
Matches 1211; Conservative 0; Mismatches 42; Indels 243; Gaps 5;

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Dh 1427 AGTGTACACCAAGAGAGTGTCTTCTGCTCCTCACCTGCCCCACTCTTACAGCTGGA 1486

REFERENCE 1 (bases 1 to 129747)
AUTHORS Wilson, S.
TITLE Direct Submission
JOURNAL Submitted (11-FEB-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
On Mar 7, 1999 this sequence version replaced gi:4176479.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence is the entire insert of clone 465N24. This sequence
has been finished according to sequence map criteria as follows. An
attempt is made to resolve all sequencing problems, such as
compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.

This sequence was generated from part of bacterial clone contigs of
human chromosome 1, constructed by the Sanger Centre Chromosome 1
Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr1>
465N24 is from the library RPCI3 constructed at the Roswell Park
Cancer Institute by the group of Pletier de Jong. For further
details see <http://pacpac.med.buffalo.edu/VECTOR>: pcrPac2.

FEATURES

SOURCE

1. 129747
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14893. 15096
repeat_region
/note="MLTID repeat: matches 286. .505 of consensus"
15159. 15484
repeat_region
/note="MLTID repeat: matches 6. .323 of consensus"
15487. 16041
repeat_region
/note="L1MC4 repeat: matches 7451. .7973 of consensus"
16069. 16773
repeat_region
/note="L1ME3A repeat: matches 3211. .3943 of consensus"
16774. 17068
repeat_region
/note="AluSg repeat: matches 3. .297 of consensus"
17071. 17384
repeat_region
/note="AluSg repeat: matches 1. .310 of consensus"
17385. 17451
repeat_region
/note="L1ME3A repeat: matches 3943. .3955 of consensus"
17567. 17775
repeat_region
/note="L1ME3A repeat: matches 4012. .4208 of consensus"
17912. 18219
repeat_region
/note="AluSg repeat: matches 1. .313 of consensus"
18401. 18922
repeat_region
/note="L1ME3A repeat: matches 4315. .4848 of consensus"
18923. 19226
repeat_region
/note="AluX repeat: matches 1. .304 of consensus"
19227. 19530
repeat_region
/note="L1ME3A repeat: matches 4848. .4586 of consensus"
19531. 19897
repeat_region
/note="L1PB1 repeat: matches 5781. .6155 of consensus"
19898. 20698
repeat_region
/note="L1ME3A repeat: matches 4585. .5403 of consensus"
21061. 21150
repeat_region
/note="MIR repeat: matches 115. .213 of consensus"
21218. 21390
repeat_region
/note="L2 repeat: matches 1626. .1814 of consensus"
21511. 21767
repeat_region
/note="L1MC4 repeat: matches 6664. .6940 of consensus"
21771. 21969
repeat_region
/note="L1MC2 repeat: matches 3850. .4054 of consensus"

repeat_region	21970..22008	/note="u2 repeat: matches 1..39 of consensus"
repeat_region	22009..22354	/note="L1MC2 repeat: matches 4054..4410 of consensus"
repeat_region	22355..22663	/note="Alusx repeat: matches 1..309 of consensus"
repeat_region	22664..23540	/note="L1MC2 repeat: matches 4410..5261 of consensus"
repeat_region	23552..23730	/note="FAM repeat: matches -135..43 of consensus"
repeat_region	23731..24657	/note="L1MC2 repeat: matches 5278..6319 of consensus"
repeat_region	24659..24758	/note="AluJ/ELAM repeat: matches 2..77 of consensus"
repeat_region	24759..25029	/note="L1MC4 repeat: matches 7461..7777 of consensus"
repeat_region	25872..26333	/note="L1MB5 repeat: matches 4928..5368 of consensus"
repeat_region	26334..26622	/note="L1MB8 repeat: matches 5995..6287 of consensus"
repeat_region	26623..26774	/note="L1MB5 repeat: matches 5368..5512 of consensus"
repeat_region	26775..27077	/note="Alusx repeat: matches 1..298 of consensus"
repeat_region	27078..27656	/note="L1MB5 repeat: matches 5512..6176 of consensus"
repeat_region	27713..27944	/note="AluJ repeat: matches 74..239 of consensus"
repeat_region	27959..28020	/note="L1MC3 repeat: matches 6941..7003 of consensus"
repeat_region	28028..28269	/note="121 copies 2 mer gg 60% conserved"
misc_feature	28146..28221	/note="tandem repeat in single clone region"
repeat_region	28512..28663	/note="L2 repeat: matches 2241..2422 of consensus"
repeat_region	29643..30184	/note="L1MR22 repeat: matches 1..505 of consensus"
repeat_region	30368..30450	/note="MIR repeat: matches 28..118 of consensus"
repeat_region	31246..31409	/note="L2 repeat: matches 1794..1967 of consensus"
repeat_region	31416..31494	/note="MIR repeat: matches 187..261 of consensus"
Query Match	13.0%	Score 260; DB 9; Length 129747;
Best Local Similarity	68.4%	Pred. No. 1,2e-61;
Batches 547; Conservative	0; Mismatches 640; Indels 113; Gaps	9

Query	Match	Local Similarity	Score	DB	Length
1221	TGCACGAGACCCAGATGTAGAGACTGGTTGGTCCCTCCCTATTTTGTCCGGAATCCAT	13.0%	260	DB 9	129747
25030	TTTCATGTGGCTGTACTAAAGTATCAGATGGCTTCACTATTTCATCC-GAATCCAT	68.4%	1,2e-61		
	Matches 547; Conservative 0; Mismatches 140; Indels 113; Gaps				
QY	1221	TGCACGAGACCCAGATGTAGAGACTGGTTGGTCCCTCCCTATTTTGTCCGGAATCCAT	1280		
DB	25030	TTTCATGTGGCTGTACTAAAGTATCAGATGGCTTCACTATTTCATCC-GAATCCAT	25088		
QY	1281	CCTAGGCCAGAAACAGCCCCAAAGGCCAGTGCAGTCTCTTTCAGCAAAAGATGTGTT	1340		
DB	25089	CCTGGGTGAGAAACAGCCCCAAGAGGAGACAGACAGCCCTTCCACGCAAAAGTGTGTT	25148		
QY	1341	AAGGACAGGCTTCGATGGGGCTGGGGGCGGCAAAATTCATCCAGCCATCAGACACT	1400		
DB	25119	AAGGCA----TCAATGGGCTGGGGCTGGGAAAAATTCATCCAGCCATCAGACCCAC	25204		
QY	1401	CATGATCCGCCATTGGCTGTTTAACCCCAAGACCAAGTTTAAGCAGAGGGTGAAGTGA	1460		
DB	25205	CATGATCCGCCATTGGCCATTAACTCCAGGCCAAAGTTTAAGCAGAGG-----	25255		
QY	1461	GACCGTGCCTTCCTCTTCACAGGCCAAGCTGACACCTTCCTGATGGAACATGTG	1520		
DB	25255	-----	25254		
QY	1521	AGTGTACCAATGGCCAGACACATGCTGTCAACTGTGTAGTCAAGGACTGTCCAGCCAG	1580		
DB	25255	-----CAACCAATTCTCTTAATCTGTAGCCAGAGGGCTGGGTAGGACAG	25295		

QY	1581	G	-TTTGGGACAGAGCGCTACTTTGGGAGCAGCCTGAGGTGTAAAGGCGAGCAACA	1637
Db	25300	GGGTTTGAAGGGGATAAACCCCTCTTCTAGAGACCACCTTGAGAGATGAAGGCGAGACACA	25359	
QY	1638	GGTGAAGGTGAGTGTGACACCAGAGAC	-TGTCTTCTGTGCCCTCACCTGCCCCATC	1695
Db	25360	GGTGAAGGTGAGTGTGACACACAGAGACTGTCTTCTGTGCCCTCACCTGCCCCATC	25419	
QY	1696	CTACAGCTGGAGC	-----TGCATGTGACCCACCTGATCTCTGTGAGAGTCT	1746
Db	25420	CCACAACTTTGGGCTTACCCTTGGAGGTGGCATTTACCGATCTCTGTGCGAGGGCT	25479	
QY	1747	GCT	-CTGTGGCAGGCTCTTGTTTATGACCATGATCAGATGTGTGCAGACTTTTCTGG	1805
Db	25480	GCTACTGTGTGATGACTCCTATTATTCAGAGCATGATCAGATATGACCAAGGCTCTCTGCT	25539	
QY	1806	CCTGAGACACACGGTCACTTGTGTACTGTCTGTGTGACACAGATGCTTGAAGCATCTCA	1865	
Db	25540	CCTGAGACACCAAGTCTTGTGTACTGTCTGTGTGACCAAAAGTGTGAGGCAATCTCA	25599	
QY	1866	GGCAGCCTCAGCCCAAGCTTCTTACTGTGCTTGTGATCTCTCTCA	-GCATAGCCTGGGCA	1924
Db	25600	GGCAGACTTAACCTGATGTTTCTTCACTGCTCTGCACTTGTCTGTAGGCATGTCTGGGCA	25659	
QY	1925	AGCAGGTTGGGAATGAGATAGCATGGATGTATGGAGAGATGAAGATTTTCCG	1984	
Db	25660	AGCAGGTTGGGAATGAGAGGAT	-----GGAGGTGTGAGAGGATGAATAATTTTCAATG	25712
QY	1985	AAAAAAAAAAAAAAAAAAAA	2004	
Db	25713	TAAACCTTTTAAAGGAA	25732	

	RESULT	13
G23637/c	LOCUS	
	DEFINITION	G23637 391 bp DNA linear STS 31-MAY-1996
	ACCESSION	human STS WI-13434 , sequence tagged site.
	VERSION	G23637.1 GI:1343963
	KEYWORDS	STS; STS sequence; primer: sequence tagged site.
SOURCE		Homo sapiens STS derived from sequences in dbEST and the Unigene collection.
ORGANISM		Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euarcharia; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE		1 (bases 1 to 391)
AUTHORS		Hudson,T.
TITLE		Whitehead Institute/MIT Center for Genome Research; Physically Mapped STSS
JOURNAL		Unpublished (1995)
COMMENT		Contact: Thomas Hudson Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research 9 Cambridge Center, Cambridge MA 02142 USA Tel.: 617 252 1900 Fax: 617 252 1902 Email: thudson@genome.wi.mit.edu Primer A: TACATGAAATTCTTCATCCTCC Primer B: CTCGTGCACCAGACTGGTTGA STS size: 150 PCR Profile: Presoak: Denaturation: Annealing: 56 degrees C Polymerization: PCR Cycles: 35 Thermal cycler: Protocol: Template: 10 ng Primer: each 5 pM dNTPs: each 4 mM

